

SEQUENCE LISTING

<110> Nicolaides, Nicholas
Grasso, Luigi
Sass, Philip
Kinzler, Kenneth
Vogelstein, Bert

<120> A method for generating hypermutable
plants

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Sequence ID 5. Human PMS134 cDNA and amino acid sequences.

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301  CAT ACT TCT AAA TTA GAG GAT TTC ACA GAT CTT TTG AAT TTG ACT ACT TAT GGT TTT AGA
    G   E   A   L   S   S   L   C   A   L   G   N   L   T   V   E   T   R   T   K
361  GGA GAA GCC TTG AGC TCT CTC TGT GCA TTG GGA AAT CTC ACT GTG GAA ACA AGA ACA AAG
    N   E   P   V   A   T   L   *
421  AAT GAG CCA GTT GCT ACG CTC ...

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Sequence ID 6. *Arabidopsis thaliana* PMS134 homologue cDNA and amino acid sequences.

1 70

humPMS2 (1) ATG GAG GAG GAT GAG AGCT CCG ACAG AAG CT G TAAG GCC ----- AT CAA CCTTAT GAT CGG AAG T

AtPMS2 (1) ATG CAAG GAG ATCTTCTCCGTC CCGACGATCTAGCTCTCTCTTGAAGACCTATTAACAGC

Consensus (1) ATG A GAG T CG T C CT CTA C AT A ACCTAT A G AA

71 140

humPMS2 (65) CAGTCCATCAGATTTCGCTGTGGCGGTGGTACTGAGTCTAAGCACTGGGCTAAGGAGCTAGTAGAGAA

AtPMS2 (71) TAAATCAGAGAATCTGTTCCGCTAAGTCACTAGAGCTCTCTTTCGGCGCTAAGGAGCTGTTCAGAGAA

Consensus (71) A T CA AT TG TC GG CA GT T T CT C GC GT AAGGAG T GT GA GT

141 210

humPMS2 (135) CAGTCTGGATGCTGGTGGCACTATATTCATCTAAGCTTAAGCACTAGAGTGGATCTATTGAGTT

AtPMS2 (141) TAGTCTGACGCGCGCGCCACCTATATAGAGATTAACTCCGAGACTACGCGAAGACTATTTCAGCT

Consensus (141) AGTCT GA GC GG GCCAC A TAT GA T AA CT GACTA GG G GA T TT A GT

211 280

humPMS2 (205) TCAGACAATGCAATGCGGCT-----AGAAGAG-----AAACTTCGAG-----G

AtPMS2 (211) ATTCAACATGCTGTGGCATTTCCCAACCAATTTCAAGTTTGTGTCCAAATCTCCGAACTTTT

Consensus (211) GACAATGG TTGG T A AAG AA CT CGAAG G

281 350

humPMS2 (246) CTTAAC-----CTCAACATCAACATCTAAGATCAAGAGTTTGCGCACTAACTCAAGCTGAA-ACT

AtPMS2 (281) ATGTTCTTGCACCTTAAGCATCATCTCTTAATTAAGAGATTTCAGAGATCTTTTGAATGTACTACT

Consensus (281) T CT CT AA CATCA AC TCTAA T A GA TT C GA CT T A TTGA ACTT

351 420

humPMS2 (311) TTGGCTTTCCGGGGGAAGCTCTGAGCTCACTTTGTGCACCTGACGATGTCACTATTCTCTCTCCAC

AtPMS2 (350) ATGGTTTTCAGAGGAAAGGCTCTGAGCTCTCTCTGTGCATTCGGAATCTCACTGTGGAATAAGAGAA

Consensus (351) TGG TTT G GG GAAGC TGAGCTC CT GTTGCA TG G AT TCAC T AC G C A

421 490

humPMS2 (379) GCATCGGCGAAGGTTTGAAGCTGACTGATGTTTGATCACAATGGGAAATTA-TCCAGAAACCCCTTAC

AtPMS2 (420) GAATGAGGCA--GTTCACGCTCTTGACGTTTGATCATTCGGTTTGGTTAATGCTGAAGAGAGACTG

Consensus (421) G AT GC A GTTG AC C TGA GTTGATCA TGG TTA T C GAAAA

491 560

humPMS2 (448) CTCGCGCCAGAGGCAACCAAGTCAAGCTGCAAGCACTTATTTCCACACTACCTGTGCCCATAAAGAA

AtPMS2 (488) CTCGCCAAATGCTACCACTCTACTCTAGCAAGTTGTTCTCTTAATTACCTGTCCAGGCAAGAG

Consensus (491) C C GCC A GG ACCAC GTCA GT G AGTT TT TC A TACCTGT CG AA GA T

561 630

humPMS2 (518) TTCAAAGGAATATTAAGAAAGAGTATGCCAAATGCTCCAGGCTTACATGCATCTGTATCATTTAGC

AtPMS2 (557) TTAAGCGGAAATATACGAAAGAAATGCGAAGCTTGTATCTTATTGAACGCATATGCGCTATTGAGAA

Consensus (561) TT A GGAATAT AA GA TATG AA T GT T TT A GCATA T ATT C

631 700

humPMS2 (588) AGGCATCGCTGTAAGTTGGCACTCACTTGGCAAGGAAGAAAGCAGGCTGTGATGCACAGGTGGA

AtPMS2 (627) ACCAGTCCGCTTTGTCTGCTTCAACACAGCTGGGAAA--AACCAAGATCTGTG--GCTGT

Consensus (631) AGG T CGG T TGC C AA G TGG AAA AA C A AG CTGT GT G GA

701 770

humPMS2 (658) AGCCCCAGCAATAAAGGAATAATATCGGCTCTGTGTTTTCGCAGAAAGCAGTTGCAAAGCCTCATTCTTTTG

AtPMS2 (686) A--CA-CAGAA-GGGA-----G-G-----G

Consensus (701) A CA CA AA GG A G G

771 840

humPMS2 (728) TTCAGCTGCCCTTAGTGACTCCGCTGTGTGAGAGTACGGTTTGGAGCTGTTCCGATGCTTCGCAATCTCT

AtPMS2 (702) TTCA-----GT-TAAGA--TAAT-----ATCATACAGTTT-----TCGGCATTAGTA

Consensus (771) TTCA C TA GA T A A AC GTTT TC GCAT A

841 910

humPMS2 (798) TTTTTACATCTCAGGTTTTCATTTTCACAATTCACGATGGAGTTGGAAAGGATTCAACAGACAGACAGTT

AtPMS2 (743) CTTTCAACAGCT-----TACA-GCTGCTACTGGACGATATTAGCAGTTCGACAGTAA

Consensus (841) TTTACA TC T CA GC TGG TGA G A TT A CAGA GACAGT

911 980

humPMS2 (868) TTTCTTTATCAACCGCGCGCTTGTACCCAGCAAAAGGCTTCGCAAGCTCGTGAATGAGGCTACACAGTGT

AtPMS2 (796) TTTCTTTAATAATGCTCGGCTGTATATATGCCAAAGATCAAGCAAGTTGGTGAATGACTATAT-AAAGAT

Consensus (911) TTTCTTTAT AA G CGGCT GA CAAA GTC GCA T GTGAATGAG T TA A A T

981 1050

humPMS2 (938) ATAA-TCGACACCACTATCCAT-TGTTGTTCTTAACTTCTGTTGATTCAGATGCGT-GATATCAATG

AtPMS2 (865) ACAAGTTCTCGGAATATCCACTACCATTCGGAATTTATCTGCGTGGTGGAGCATG-GATTTCAGATG

Consensus (981) A AA T C A TATCCA TT TTCT A TT TGT T G A TGAT T AATG

1051 1120

humPMS2 (1007) TTACTCCAGATAAAAGGCAATTTTGGTCAACAAGGAAAGCTTTTCTTGGCACTTTAAAGACCTCTTT

AtPMS2 (935) TACGCGCCGATAAAAGAAAGGCTTCTTTTCTCAGCA--CTTCTGTTATCGTT-----CTTT

Consensus (1051) T AC CC GATAAAG A T TT T GA GA A CTT TGTT G GTT CTTT

1121 1190

humPMS2 (1077) GATACGAATGTTTGTATAGTGATGTCAAGAGCTAAATGTGAGTCAGCAGCCAGTGTGTGATGTTGAAGGT

AtPMS2 (993) GAG-GGAAGCTTCGA-----A-CGATATATTCG--T-----CCAGTAATCGCTCTAT--

Consensus (1121) GA GGAA GT TGA A C AG TA AT C T CCA T TG T TT A

1191 1260

humPMS2 (1147) AACTTAATAAATAATCATGCAGCGGATTTCGAAAGGCCATGTTAGAAAGCAGGATCATTCCTCTGAT

AtPMS2 (1040) ---TGTATATAGCTTCGAGCAATTCGAGGCAACC--AGATAAG---GCGTGGTTCGCTG

Consensus (1191) T T AA A T G G G ATT GGA A CC AGA AAG G T A C T C T

1261 1330

humPMS2 (1217) TAAGGACTGGAGAAGAAAAAAGACGCTGTCATTTCAGACTTCAGAGGCGCTTTTCTCTCTCTCAC

AtPMS2 (1097) TTC-----AAGAAGAAATCAAA--TCTTTTGTCAAG--GGGATAG-----TTCGTGATTCAGT

Consensus (1261) T AGAAGAAA AAA TC TT CAGA G GA AG TTCT GTCA 1400
 1331
 humPMS2 (1287) AACAGAGAACAGCCTCACAGCCCAAGACCCAGAACCAAGAGGAGCCCTCTAGGACAGAAAAGGGGT 1400
 AtPMS2 (1148) CTAA---AACAGACT---AGGGGAAGCTATGAGAGAGAAATCCCTCTAAGGGAGTTGAAATTGA
 Consensus (1331) A AACAG CT AGG AA T AGAA AA A A CC T GGA AA G
 1401 1470
 humPMS2 (1357) ATGCTGTCTTCTAGCACTTCAAGTCCCATCTCTACAAAGGCGTCCTGACAGCTCAGAAAGAGGCAGTGA
 AtPMS2 (1212) TAATAGTTCGCGATGGAGAAGTTAAGTTTGAATGAGGCAATG-TGGCAGCA-ACAAACGGCAAG---
 Consensus (1401) GT C A AG T T T GA AAGGC T TG GAC AGAAAG GG AG
 1471 1540
 humPMS2 (1427) GTTCAGTTCACGAGCCAGTGACCCCTACGACAGAGCGGAGGTGGAGAAAGACTCGGGGCAAGCAGCAC
 AtPMS2 (1277) GTTCT--TTT---CAGT---CCAT--GATGTATTCACCTTCACAAAG-ACACCTAGCAAAAGTTTGG
 Consensus (1471) GTTC T A CAGT CC GA A C A T GA AAG AC C GCA G C
 1541 1610
 humPMS2 (1497) TTCCCTGGATTCGAGGGGTTTCAGCATCCAGACACGGGCGAGTACTGACAGCAGAGTATGCGGCGCGC
 AtPMS2 (1334) CTCAGTTAATCTGACTG-----AGA-----AGTTACTGATGCA--AGTA-----TAG
 Consensus (1541) TC GT A T TGA G AGA AGT ACTG GCA AGTA A
 1611 1680
 humPMS2 (1567) TCCCAAGGGGACAGGGGCTCGCAGGACACCTCTGACTCTCAGGAGAAAGCGCTGAAACTGACCACTCTT
 AtPMS2 (1376) AGTTGAG---CAGCCCTCT---A-GCTTGGCCAGTCA-----ACTT---TGAATACTTTT
 Consensus (1611) C AG CAG GCTC A T TG C TCA CT TGA ACT TT
 1681 1750
 humPMS2 (1637) TTTCAGATCTGGACTGCCATTCAAAACAGGAAGATCTCGGATCTAAATTTTCAGAGTTTGGCTCAGCCAAAC
 AtPMS2 (1423) GTTACCATGGG-----AAA-----AAGAAAG--ATCAAAA-----CATAGCC--AG
 Consensus (1681) TT ATG G AAA AAGA A C ATG AAA C T AGC AC
 1751 1820
 humPMS2 (1707) TAATCTCGAACCCTCAACACAAAGCGTTTAAAAAAGAGAAATTCCTTCCAGTTCTGACATTTGTCAA
 AtPMS2 (1461) CATCTCTCTG-----AAACACCT---GTCCACAGAAACCA-AACTTC---AGTTAT---CGTCTGGAGA
 Consensus (1751) A CTC C AAAC C GT T A AAA A AA TTCT AGTT T C T TG A
 1821 1890
 humPMS2 (1777) AAGTTAGTAAATACTCAGGACATCTCAGCCTCTCAGGTTGATGTAGCTGTGAAATTAATAAGAAAGTTG
 AtPMS2 (1517) AA---AGCAAA-TTGAAGTTCTGTC-----CTTAGCTTCA--AGGTCG---CCCGT---GCAAGCGC
 Consensus (1821) AA AG AAAT AG C TG CT AG TT A AG TGT T T G AAG G
 1891 1960
 humPMS2 (1847) TGCCCTGGACTTTTCTATGACTTCTTTAGCTAAACCAATAAAGAGTTTACATCATCAAGCACAGCAAAAG
 AtPMS2 (1568) ATCAACTTGA---GATATG-C---TCTCTCAAAG-----GAGATATGACCAAGGG---AAAG
 Consensus (1891) C CT GA T TATG G T A CT AA G G AG TA CA AAGC AAAG
 1961 2030
 humPMS2 (1917) TGAAGGGGAACAGAAATACAGCAAGTTTAGGCAAGATTTCTCCTGGAGAAATCAAGCAGCCGCAATAT
 AtPMS2 (1620) ACATTTCTAACT-----ACCAATC---GATTTCTCCTGGAAAC---CAAGCTCATAATCTT
 Consensus (1961) GA GAAC AGG A T G GATTT TCTTGA A CAAGC G A G T
 2031 2100
 humPMS2 (1987) GAACTAAGAAAGAGATTAATAAAAGATGTTTGCAGAAATGGAATCATTTGCTCAGTTTAACTTGGAT
 AtPMS2 (1672) GAA---AGACATGAGACA-ATA---C-----CCGGCAATTCAATCTTGGGT
 Consensus (2031) GAA AGA A GAGA A GTA C T GG CA TT AA CT GG T
 2101 2170
 humPMS2 (2057) TATATAACCAAACTCAATGAGGATATCTTCATAGTGGACCAAGCATGCAAGGACGAGAAATATACTTT
 AtPMS2 (1712) TCACTATTGCAAAATTTGAGCGAGATCTGTTCAATCTGGATCAGCATGAGCTGATGAGAAATTCACCTT
 Consensus (2101) T AT AT C AAA TG A GAT T TTCAT GTGA CAGCATGC C GA GAGAA T AACTT
 2171 2240
 humPMS2 (2127) CGAG-ATGCTGCAAGCAGCAACCTGCTCCAGGGGCGAGGCTCTAGCA-CCTCAGACTCTCACTCTAA
 AtPMS2 (1782) CGAATTTTGAAGGTCACACTGCTGAAACCAACG-ACCTTACTCAGCCTTTTAACTTGGAGCTCT
 Consensus (2171) CGA AT GCA CA AC GT CT A GCA A CT A CA CCT GA T A T
 2241 2310
 humPMS2 (2195) CTGCTCTTAATGAAGCTGTCTCTGATGAAATCTCGGAATATTTAGAAACCAATGGCTTTGATTTCTTTAT
 AtPMS2 (1850) CTCACAGACAGAAAGTAACCTCTTTAATGCACTGGCTATTATCAGGGGAAATGGCTTTCTTCTAGAGGA
 Consensus (2241) CT C G A GAAG T TG TA A TGA AT T AG A AATGGCTTT T T G
 2311 2380
 humPMS2 (2265) CCATGAAATGCTCCAGTCACTGAAAGGGCT--AAACTGATTTCCTTGCCAACTAGTAAAACTGGACCT
 AtPMS2 (1920) GAATCCAACTGCTCC--TCCGGGAAACACTTTAGCTACGAGCGATTCGTTATAGCAAGATATCACCT
 Consensus (2311) AT AA TGCTCC TC C GAAA CT A ACT CC T CC TAG AA AA ACCT
 2381 2450
 humPMS2 (2333) TCCGACCCGAGGACGTGATGAAGTATCTTCTCTGAGCAGACCCCTCGGG-----TCATGTGCGCG
 AtPMS2 (1988) TTGGAGTCCAGATCTTAAAGACTGATCTCACTCTAGGAGATACCATGGGGAAATGTTTGGGTGCTAG
 Consensus (2381) T GGA C A GA T A GA CTGATCT A CT G A G A CC TGGGG TC TGC G
 2451 2520
 humPMS2 (2398) -----CCTTCCGAGTGAAGCAGATGTTTGGCTCCAGAGCC
 AtPMS2 (2058) TAGCTACAAAACAGCAAAACAGATTCGATTGTCCATCAGAGTCCGTCATATGCAATCCGAGGA
 Consensus (2451) CC TC CGAGTC ATG T GC TCC GAGC
 2521 2590
 humPMS2 (2434) TCCCGAACTCGGTGATGATTTGGGACTCTCTTAAACCAAGCGAGATGAAGAACTGATCACCACATGG
 AtPMS2 (2128) TCGCATCATCTGTGATGATCCGAGATCCACTCAGAAATAACCAATGCAAGATAGTGAACACTTGG
 Consensus (2521) TGC G TC GTGATGAT GG T C CT A A AA CGA ATG AGAA T T CAC TGG
 2591 2660
 humPMS2 (2504) GCGAGATGACCAACCCCTGGAACTGTCCCATGGAAGGCCAACCATGAAACACATCCCAACCTGGGTGT
 AtPMS2 (2198) CAGATCTCGAATCTCCTTGAATTCGCCACACCGAACCAACCAATGCTCATCTTTGGACTTCACAA-
 Consensus (2591) GA T GA CC TGGAA TG CC CA GGA G CCAAC ATG G CA T G AC TG